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Nonenzymatic extraction of cells from clinical tumor material for analysis of gene expression by two-dimensional polyacrylamide gel electrophoresis

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We have compared different methods of preparation of malignant cells for two-dimensional electrophoresis (2-DE). We found all methods using fresh tissue to be superior compared to methods using frozen tissue. Our results indicate that nonenzymatic methods of preparation of tumor cells, including fine needle aspiration, scraping and squeezing, have advantages over methods using enzymatic extraction of cells. Nonenzymatic methods are rapid, appear to reduce loss of high molecular protein species, and alleviate the necessity of separating viable and nonviable cells by Percoll gradient centrifugation. Using these techniques, high-quality 2-DE maps were derived from tumors of the lung and breast. In the resulting polypeptide patterns, heat shock proteins, non-muscle tropomyosins and intermediate filament were identified. We conclude that nonenzymatic extraction of malignant cells from fresh tumor tissue improves the possibilities that these techniques may be useful in clinical diagnosis.

1 Introduction

Tumors may develop by a number of different mechanisms in any given cell type. At the time of diagnosis, tumors will have progressed along different pathways to various stages of malignancy. To provide a basis for individual therapy it is of importance to examine specific properties of the tumor cell population in each patient. A large number of different markers have been described in order to increase the diagnostic accuracy. It is likely that a combination of several markers is needed in the future in order to reflect different properties of the tumor. One important method for the resolution of a large number of potential markers is two-dimensional electrophoresis (2-DE). Extensive efforts are being made in identifying various polypeptides separated by 2-DE and to characterize how the expression of these polypeptides is affected by the response to cellular transformation and various culture conditions [1,2]. It would be of value to transfer this information to 2-DE separations of polypeptides from tumor tissue samples. However, one prerequisite is that the quality of the 2-DE gels from tumor samples is comparable in quality with 2-DE gels from samples of cultured cells.

Frozen tumor tissues are commonly used for various biochemical assessments. However, if such samples are analyzed by 2-D polyacrylamide gel electrophoresis (PAGE), the polypeptide patterns are obscured by contamination of serum- and connective tissue proteins. Such nontumor-cell-related variations represent serious problems in the interpretation and inter-patient comparison of 2-DE

patterns [3]. 2-DE patterns of cells prepared from fresh tumor material were analyzed after enzymatic extraction of tumor cells [4, 5] or after culturing tumor fragments in medium containing radioactive amino acids [6]. These procedures may, however, lead to alterations in the gene expression/polypeptide patterns. We are only aware of one study where nonenzymatic extraction of cells from fresh tumor tissue (prostate cancer) was used to prepare samples for 2-D PAGE [4]. We have examined enzymatic extraction and various nonenzymatic preparation techniques, including fine needle aspiration, for the preparation of cells from fresh tumor tissues. We describe nonenzymatic extraction procedures that are rapid, lead to high-quality 2-DE patterns, and that alleviate the necessity to purify tumor cell populations from dead cells.

2 Materials and methods

2.1 Cell cultures and samples used for spot identification

A rat embryonal fibroblast cell line, WT2 (a kind gift from Dr. J. I. Garrels and Dr. S. Pattersson) was used for the identification of a number of heat shock and structural proteins. Human normal diploid lung fibroblasts, WI38, human epithelial breast carcinoma cells, MDA-231 and MCF-7 were purchased from ATCC and grown as recommended. Polypeptides prepared from a leukemia type pre-B-ALL were separated by 2-DE. The 2-DE map was then analyzed by Dr. S. M. Hanash (University of Michigan, Ann Arbor, USA).

2.2 Tumor tissues samples

In this study, 2-DE maps from seven tumors were used as representative illustrations: two adenocarcinoma of the lung (LA, and LB, mucinous, both cases intermediate grade of differentiation), one squamous carcinoma of the lung (LS), one carcinoid-like breast cancer (BC), one microfollicular adenoma (highly differentiated) of the thyroid (TA), one highly differentiated hyperneph-

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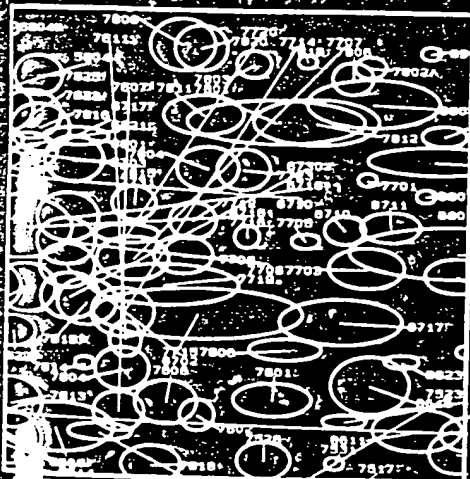
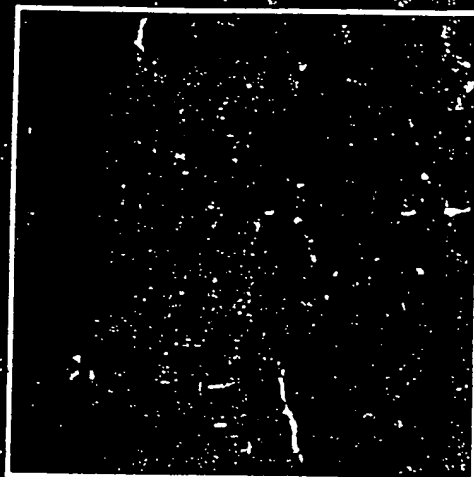
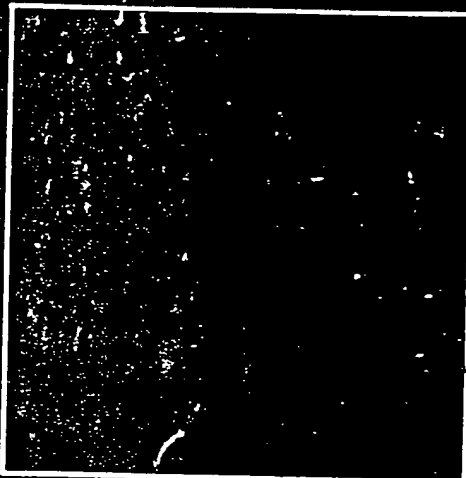
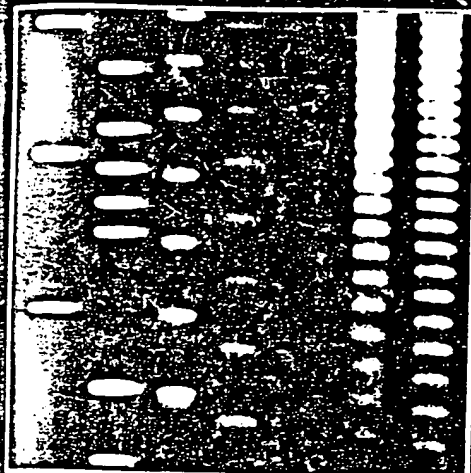
Abbreviations: 2-DE, Two-dimensional polyacrylamide gel electrophoresis; IEF, isoelectric focusing; LDH, lactate dehydrogenase; NP-40, Nonidet P-40; PBS, phosphate buffered saline; PCNA, proliferating cell nuclear antigen; PIH, protease inhibitors; PMSF, phenylmethyl sulfonyl fluoride; SDS, sodium dodecyl sulfate; WW, wet weight

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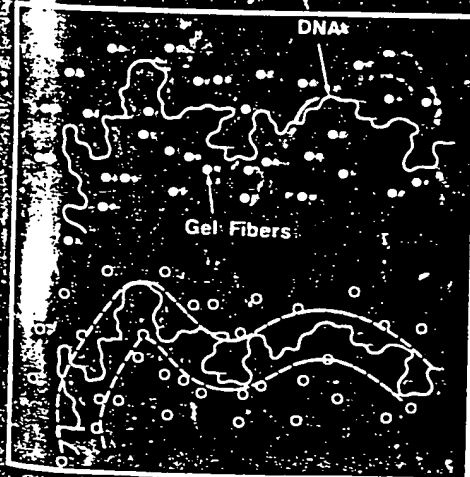
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roma, a tumor of the kidney (KH), and finally one case of poorly differentiated corpus carcinoma (CP).

2.3 Preparation of cultured cells

The cell monolayers were washed twice in phosphate buffered saline (PBS) and then scraped off in ice-cold PBS including protease inhibitors (PIH), phenylmethylsulfonyl fluoride (PMSF) 0.2 mM and 0.83 mM benzamide pelleted at $660 \times g$, 3 min ($+4^{\circ}\text{C}$) and washed one time before final centrifugation at $2700 \times g$, 5 min. The wet weight of the cell pellet was recorded and the cells were stored at -80°C until further processing.

2.4 Preparation of tumor tissue samples

2.4.1 General remarks

Macroscopically representative and non-necrotic tumor tissues were selected within 20 min after resection. Parallel samples were routinely prepared for cytology. The samples were processed as rapidly as possible on ice or at $+4^{\circ}\text{C}$ and in the presence of PIH. Cells were stained with DiffQuick (Baxter) and usually examined at three different occasions during the preparation procedure: (i) cytology sample, (ii) extracted cells and (iii) cells after percoll gradient centrifugation.

2.4.2 Specimen acquisition

The strategy of sample preparation is shown in Fig. 1. Tumor tissue cell samples were usually obtained by fine needle aspiration (NA) using a 0.7 mm needle. The syringe was filled with 1–2 mL of ice-cold culture medium/PIH. We found that if a tumor appeared to be very fibrous it is difficult to extract enough cells for 2-DE analysis. In these cases, two alternative techniques were examined. (i) The tumor was cut in the middle and the fresh surface scraped (SC) by a scalpel. The cell-rich material was then transferred to ice-cold culture medium (L15 with 5% fetal calf serum)/PIH. (ii) A part of the tumor sample was placed in culture medium on ice for further processing at the laboratory in the following way: the material was cut into very small fragments on a pre-cooled dissection plate and transferred to a small glass chamber with a 0.7 mm metal net 5 mm above the bottom of the chamber. Medium /PIH was added to cover the sample (8 mL) which was gently squeezed (SQ) towards the net in order to release and wash out cells. NA and SC were also compared with an enzymatic extraction (EE) procedure described previously [5]. Briefly, thin slices of tissue were incubated with collagenase (1 mg/mL) and elastase (2 mg/mL) in medium for 1 h at 37°C . Extracted cells from every sample were then subjected to percoll gradient centrifugation (Section 3.2.3).

2.4.3 Separation of cells by Percoll gradient centrifugation

The cell suspension was filtered through two nylon mesh filters, (i) $250 \mu\text{m}$ and (ii) $100 \mu\text{m}$ and then centrifuged

at $660 \times g$ for 3 min. The cell pellet was resuspended carefully in medium, using a syringe and loaded onto a two-step discontinuous Percoll/PBS gradient, 20.4 (density = 1.03 g/mL) and 54.7% (density = 1.07 g/mL), and centrifuged at $1000 \times g$ for 15 min. In this system, dead cells stay on the top, viable cells sediment to the interphase and erythrocytes sediment to the bottom. The viability of cells in the top fraction and interphase was checked by the trypan blue exclusion test. The interphase cell layer ($> 90\%$ viability) was collected and washed one time in a large volume PBS/PIH (centrifuged at $800 \times g$ for 3 min). Finally, the cells were resuspended in 1.4 mL PBS and pelleted at $2700 \times g$ for 5 min. The wet weight (WW) was recorded and the pellet was then stored at -80°C .

2.4.4 Final preparation of cells for 2-D PAGE analysis

From this point, cultured cell samples were treated in the same way as tumor cell samples: Each cell pellet was thawed on ice and resuspended in $1.89 \mu\text{L}$ mQ water per mg WW ($= 1.89 \times \text{WW}$) μL . The suspension was frozen and thawed 4–5 \times to break the cells [7]. A volume of $(0.089 \times \text{WW}) \mu\text{L}$ 10% sodium dodecyl sulfate (SDS), including 33.3% mercaptoethanol, was mixed with the sample and incubated 5 min on ice with $(0.329 \times \text{WW}) \mu\text{L}$ of a solution of DNase I (0.144 mg/mL 20 mM Tris-HCl with 2 mM $\text{CaCl}_2 \times 2\text{H}_2\text{O}$, pH 8.8) and RNase A (0.0718 mg/mL Tris) [8,9]. The sample was frozen and lyophilized. Sample buffer [10] including

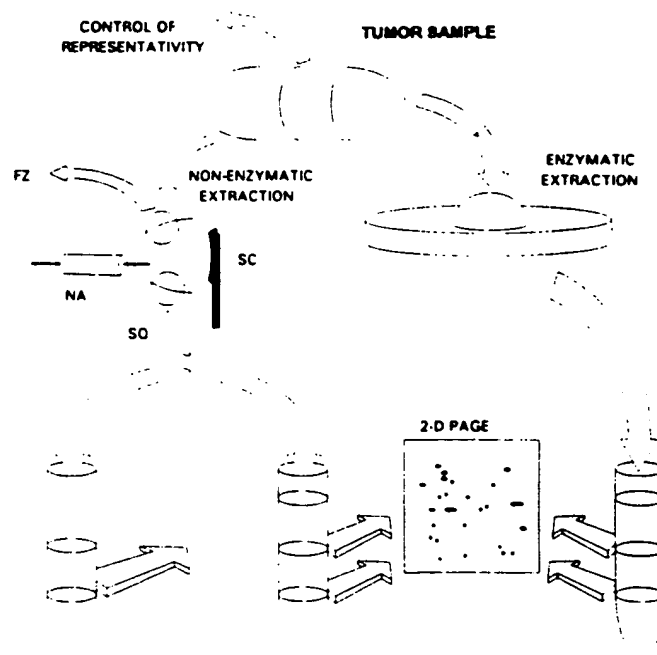


Figure 1. Experimental flow chart showing main steps of the preparation procedures. The abbreviations used for nonenzymatic extraction procedures are: FZ: frozen sample preparation; NA, needle aspiration; SC, scraped; and SQ, squeezed sample. Extracted cells are then loaded as a suspension (top volume of each tube) onto either 1.07 g/mL Percoll (left), or a discontinuous Percoll gradient from the nonenzymatic extraction (middle), or from enzymatic extraction (right). Cellular top- and interphase fractions are then used for 2-DE. For details see Section 2.

PMSF (0.2 mM), EDTA (1.0 mM), 0.5% Nonidet P-40 (NP-40), and 3-[3-cholamido propyl]-dimethylammonio]-1-propane sulfonate (CHAPS; 25 mM) was added carefully, mixed for 2.5 h and centrifuged for 15 min at

10000 rpm to remove any insoluble material. Duplicate or triplicate samples were taken for protein determination [11]. Samples were stored at -80°C prior to isoelectric focusing (IEF).

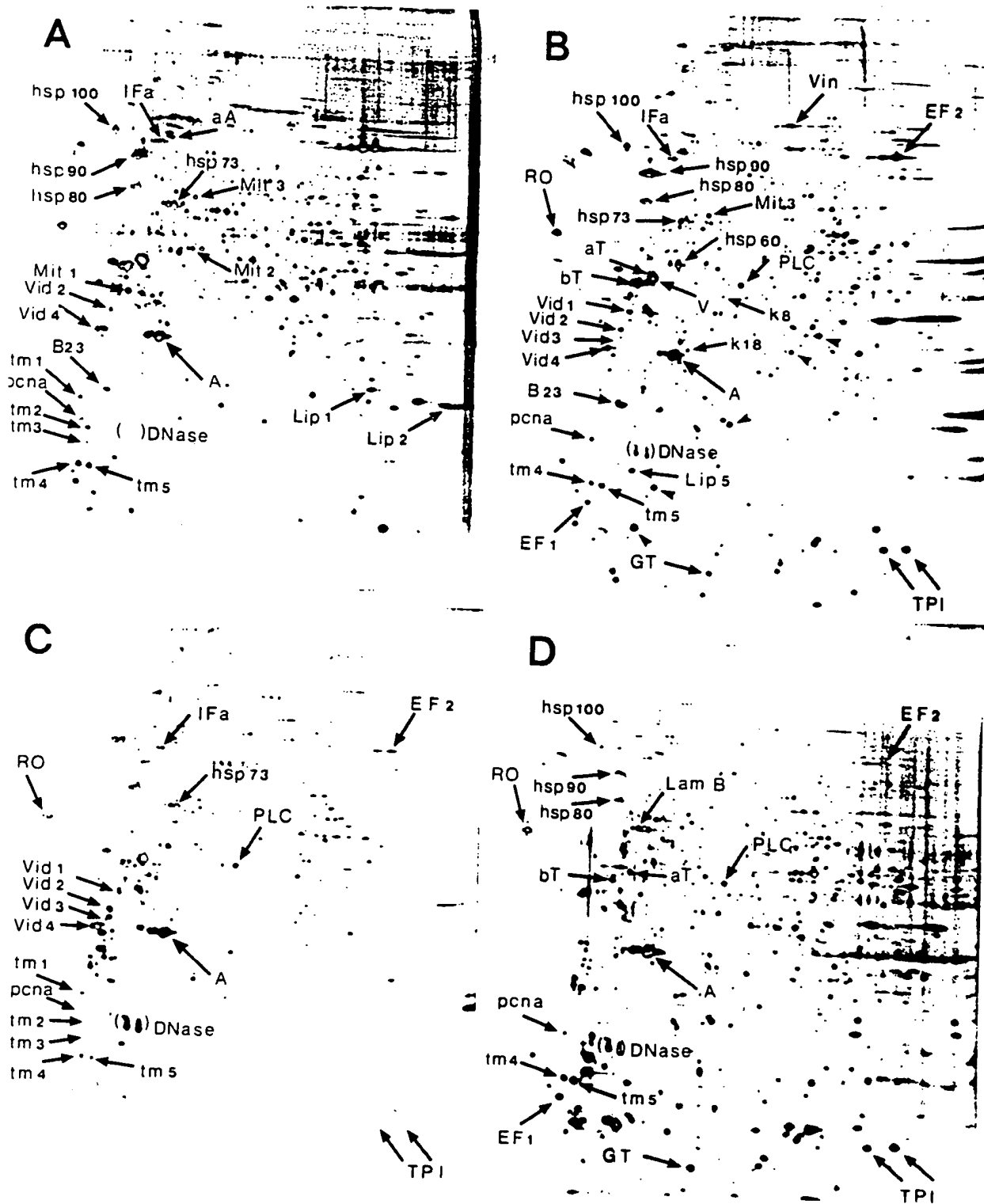


Figure 2. 2-DE analysis of samples from three cell lines and one leukemia used for the identification of polypeptides: (A) WT2; (B) MDA-231, arrowheads mark some low molecular weight cytosolic polypeptides; (C) WI38 and (D) pre B-ALL. The abbreviations for identified spots are explained in Table I.

2.4.5 Preparation of frozen tumor tissue

The technique has been described previously [3,12]. Briefly, the sample is moarted frozen to a fine powder, homogenized, lyophilized and solubilized in sample buffer.

2.4.6 Control of representativity

The tumors were examined routinely by experienced pathologists and smears or imprints from the samples were also assessed for cytometric DNA content by microspectrophotometry.

2.5 2-D PAGE

2-D PAGE was performed as described [8,10] except for the following details. The glass tubes for IEF, 1.2 × 200 mm, contained 2.0% Resolyte, pH 4–8 (BDH) and were cast to a height of 180 mm. A stock solution of acrylamide (Serva) and *N,N'*-methylenebisacrylamide (16.7:1 for IEF and 37.5:1 for the second dimension) was deionized by mixing with 5% w/v Duolite MB 5313 mixed-resin ion exchanger (BDH) for 30 min, filtered (with a 0.22 µm nitrocellulose filter) and stored at –70°C. *N,N'*-Methylenebisacrylamide, *N,N,N',N'*-tetramethylethylenediamine (TEMED) and ammonium persulfate were purchased from Bio-Rad. IEF tubes were prefocused at 200 V in 60 min. To each tube a sample corresponding to 20–40 µg protein was applied and focused for 14.5 h at 800 V and finally 1.0 h at 1000 V using a Protean II cell (Bio-Rad) and Model 1000/500 Power Supply (Bio-Rad). The tube gels were finally extruded into 1.25 mL equilibration buffer, containing 60 mM Tris, pH 6.8 (2% SDS, 100 mM dithiothreitol and 10% glycerol), frozen on dry ice and stored at –70°C. The second dimension (1.0 × 180 × 90 mm) of the acrylamide concentration was 10%

T. and the gel contained 376 mM Tris, pH 8.8, and 0.1% SDS. IEF gels were applied on top of the slab gel, sealed with 0.5% agarose containing electrophoresis running buffer (60 mM Tris-base, 0.2 M glycine and 0.1% SDS) and electrophoresed with 10–11 mA per gel (constant current) at +10°C. Six gels were run together in a Protean II xi 2-D Multi-Cell (Bio-Rad). Proteins were visualized by silver staining and photographed with the acidic side to the left [13,14].

2.6 Identification of polypeptides

Vimentin and vimentin-derived polypeptides were identified by extraction of an MDA-231 cell lysate with 0.6 M KCl/0.5% NP-40 [15]. Tropomyosins were extracted from MDA-231 and WI38 cell lysates [16], and cytokeratins were extracted from MDA-231 and MCF-7 cell lysates [17]. The patterns were compared with published maps [19–21]. Proliferating cell nuclear antigen (PCNA) was identified by immunoblotting (PC10 mAB, Dako-patt) using a semidry system (Multiphor II Nova Blot, Pharmacia-LKB Biotechnology AB) and enhanced chemoluminescence (ECL) detection (Amersham).

3 Results

3.1 2-DE of samples prepared from normal and tumorigenic cultured cells

The object of this study was to develop methods for preparation of 2-DE maps from human tumor tissue which have the same high resolution as those obtained from cultured cells. Shown in Fig. 2 are high resolution 2-DE gels prepared from cultured cells and one leukemia: SV40 transformed embryonal rat fibroblasts WT2 (Fig. 2a); human MDA-231 breast carcinoma cells (Fig. 2b); human WI38 fibroblasts (Fig. 2c) and human pre B-ALL

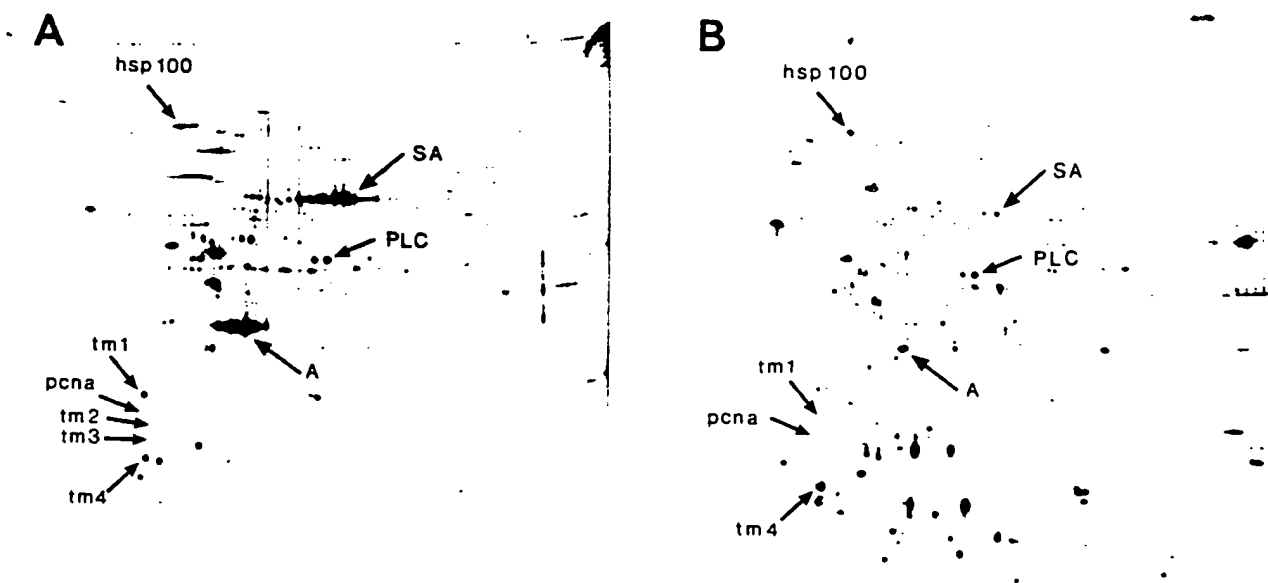


Figure 3. 2-DE analysis of a case of lung adenocarcinoma (LA). Comparison of 2-DE gel quality between (A) frozen and (B) fresh (needle aspiration) tissue preparation.

cells (Fig. 2d). Polypeptides were identified through a laboratory exchange of cell samples/2-DE maps and through 2-DE analysis of purified proteins (Table 1).

3.2 Preparation of samples from solid tumors

3.2.1 Fresh versus frozen tissue

An adenocarcinoma of the lung (LA) was prepared for 2-DE by conventional methods using frozen material (Fig. 3a). There are several possibilities for the poor resolution using frozen tissue, including the presence of high molecular weight protein aggregates. Filtering extracts through 0.1 μ m filters (Durapore, Millipore) resulted in a slightly improved resolution (not shown). When fresh tumor tissue from tumor LA was used for sample preparation, using fine needle aspiration to collect the cells, the resolution was considerably improved (Fig. 3b). The use of fresh tissue resulted in a general increase in resolution, which was most pronounced in the 50–100 kDa molecular mass range. A number of differences in the protein profiles of the gels in Figs. 3a and 3b can be observed, some of which are indicated in the figures. The decrease in serum albumin in Fig. 3b is likely to result from loss of serum proteins occurring when cells were pelleted after aspiration. Other differences, such as the decreased level of transformation-sensitive tropomyosins (TM1-TM3), may result from enrichment of tumor cells in the sample of Fig. 3b. Fine needle aspiration, a well-established technique in cytology, extracts mainly tumor cells because of decreased intercellular adhesiveness of neoplastic cells as compared to normal tissue. Microscopic examination of Diff-Quick-stained extracted cells from case LA revealed almost 100% tumor cells, whereas the whole tissue extract contained approximately 60% tumor cells.

Table 1. Names and abbreviations for identified spots

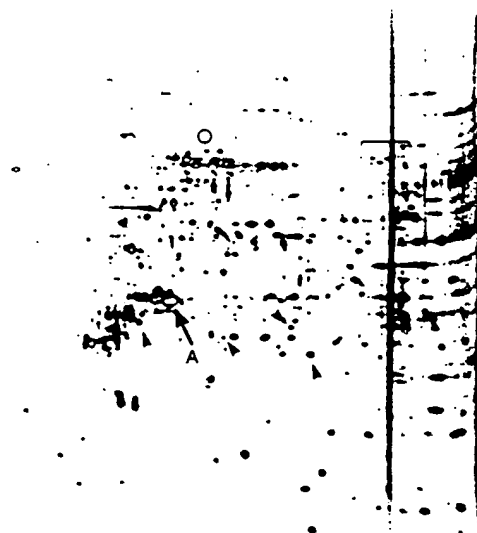
Spot	Name	Basis for identification
A	Actins	a
aA	α -Actinin	a
B23	Protein B23 /Numatrin	a
EF2	Elongation factor 2	a
EF1	Elongation factor 1 β	a
GT	Glutathione-S-transferase (<i>pi</i>)	a
hsp60	Heat shock protein 60	a
hsp73	Heat shock protein 73	a
hsp80	Heat shock protein 80, GRP78, BIP	a
hsp90	Heat shock protein 90	a
hsp100	Heat shock protein 100, Endoplasmic	a
IFa	Intermediate filament associated	a
k8	Cytokeratin 8	b and a
Lamb	Lamin B	a
Lip1	Lipocortin I	a
Lip2	Lipocortin II	a
Lip5	Lipocortin V	a
Mit1	Mitcon 1/ β - F1 ATPase	a
Mit2	Mitcon 2	a
Mit3	Mitcon 3	a
MRP	Mucine Related Polypeptides	—
pca	Proliferating cell nuclear antigen	c and a
PLC	Phospholipase C (1)	a
RO	RO/SS-A antigen	a
SA	Serum Albumin	b and a
aT	α -Tubulin	a
bT	β -Tubulin	a
tm1	Non-muscle tropomyosin isoform 1	b and a
tm2	Non-muscle tropomyosin isoform 2	b and a
tm3	Non-muscle tropomyosin isoform 3	b and a
tm4	Non-muscle tropomyosin isoform 4	b and a
tm5	Non-muscle tropomyosin isoform 5	b and a
TPI	Triose phosphate isomerase	a
V	Vimentin	b and a
Vid1	Vimentin derived protein	b and a
Vid2	Vimentin derived protein	b and a
Vid3	Vimentin derived protein	b and a
Vid4	Vimentin derived protein	b and a
Vin	Vinculin	a

a. homologous position with respect to other mammalian systems

b. purified protein(s)

c. immunoblotting

A



B

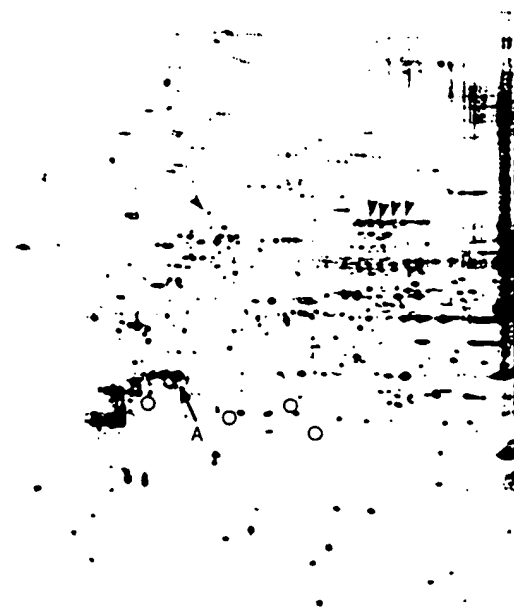


Figure 4. 2-DE analysis of a case of breast carcinoma (BC). Comparison of 2-DE quality and some differences in detected spots (arrow heads indicate increased intensity and circles or bracket indicate decreased intensity of the same spots) between (A) enzymatically and (B) nonenzymatically (scraped) tissue preparation.

3.2.2 Comparison of different methods for preparing cells from fresh tumor tissue

Samples were prepared from breast and lung carcinomas using either an enzymatic treatment with collagenase/elastase or using nonenzymatic preparations (Fig. 4). A number of differences in the protein profiles were observed in the resulting 2-DE gels, some of which are indicated in Figs. 4a and b. These differences include both increases and decreases in spot intensity. These differences may result from degradation of high molecular weight polypeptides during enzymatic treatment, increased solubilization of polypeptides, or may have other causes. For many tumors, it was only possible to obtain

small amounts of material since they were reserved for other examinations. In these cases, samples could be prepared for 2-DE using either needle aspiration or scraping. Figure 5a shows a 2-DE gel prepared from squamous lung carcinoma (LS) cells collected by needle aspiration and Fig. 5b shows a gel prepared from the same tumor by scraping. In this case, a number of differences were recorded between the two procedures, some of which are arrowed in Fig. 5. Samples obtained from other tumors (breast and lung) generally showed fewer differences between these two methods of cell sampling (not shown). These data show that different nonenzymatic extraction procedures may yield different polypeptide patterns. However, the number of spots with a large

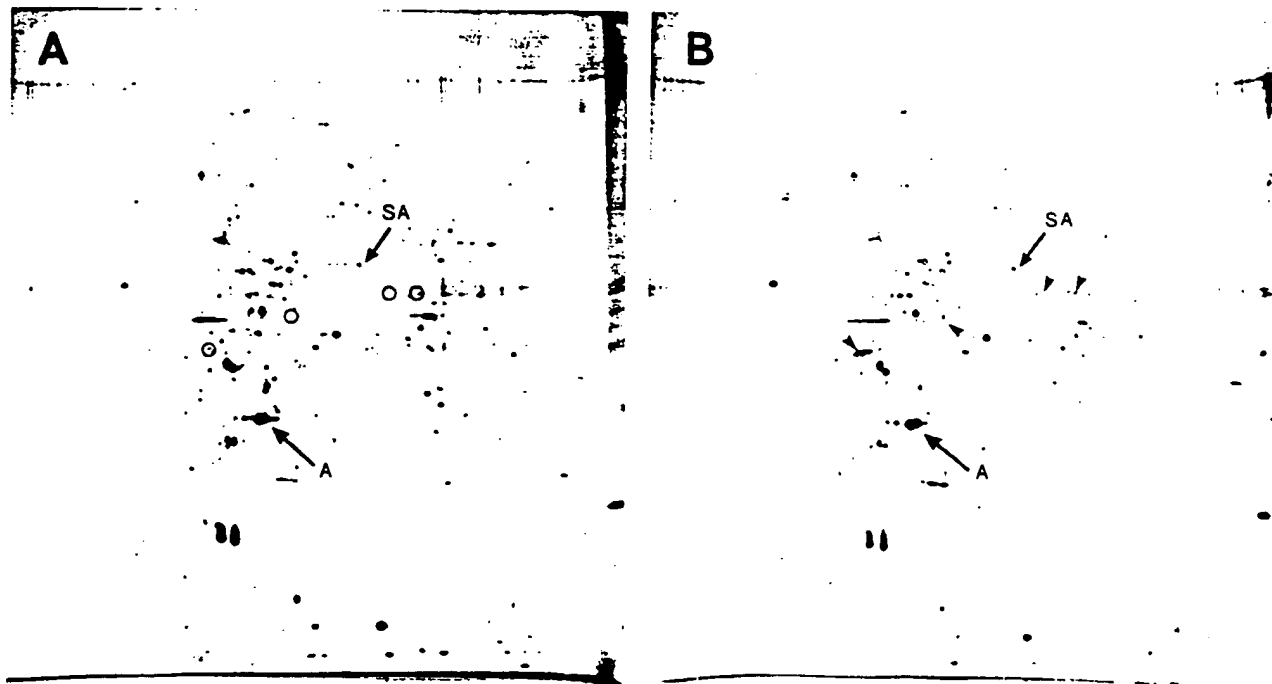


Figure 5. 2-DE analysis of a case of lung cancer (LS). Comparison of 2-DE gel quality and detected spots (arrow heads and circles) between (A) aspirated (needle aspiration) and (B) scraped preparations from fresh tissue.

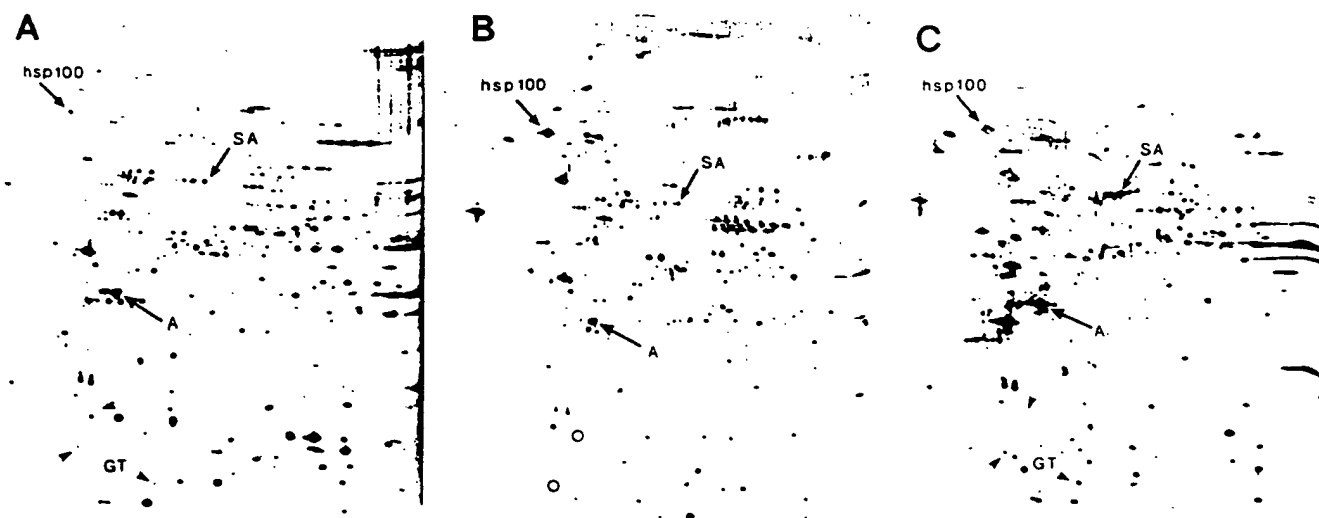


Figure 6. 2-DE analysis of three other types of tumors, (A) hypernephroma, (B) an adenoma of the thyroid and (C) corpus cancer, using the nonenzymatic preparation technique. Arrowheads and circles indicate some cytosolic polypeptides.

difference in intensity were lower than when a nonenzymatic preparation was compared with an enzymatic preparation.

2-DE maps of satisfactory quality were prepared by a third procedure. Cells were released from small pieces of tumor by squeezing (see Section 2). Some examples of this are shown in Fig. 6 where 2-DE maps derived from a case of hypernephroma, KH (Fig. 6a), a case of thyroid tumor, TA (Fig. 6b) and a case of corpus cancer, CP (Fig. 6c) can be seen. We conclude that nonenzymatic techniques are useful for 2-DE analysis of a number of different tumors. The quality of the resulting gels is com-

parable to that obtained using cultured cells (compare the gels in Fig. 2 with those in Fig. 4, 6 and 7). Which of these methods will be optimal will, in our experience, depend on the tumor material. For example, very small tumors are preferably extracted by squeezing; on the other hand, breast cancers (which are often fibrous) yield satisfactory samples using scraping.

3.2.3 Purification of cells on percoll gradients

We considered the possible advantage of separating viable cells from dead cells, erythrocytes, and debris using discontinuous Percoll gradients. Cells collected

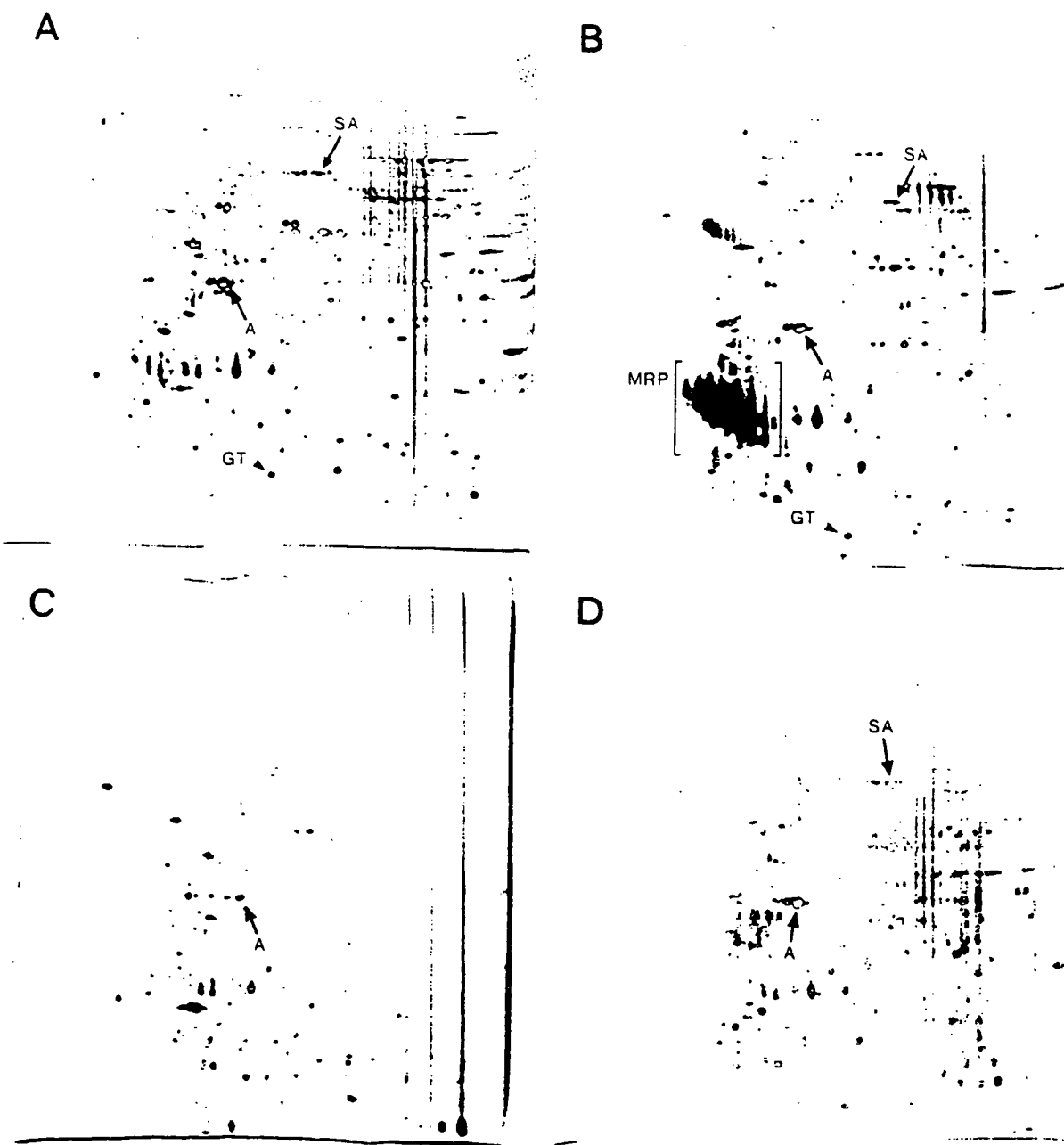


Figure 7. 2-DE analysis of polypeptides from viable (b and d) and nonviable (a and c) cells of an adenocarcinoma of the lung (LB), separated using discontinuous Percoll density gradient. Nonenzymatic preparation technique (a and b) and enzymatic preparation technique (c and d) are compared.

from the interphase showed a viability of more than 90% as judged by trypan blue exclusion test. However, it was found that the yield of viable cells decreased dramatically if the tissue resection was not immediately processed. To study the effect of lysis of cells during the preparation procedure, 2-DE maps were prepared from nonenzymatically extracted cells of case LB collected from the top fraction (nonviable, Fig. 7a) and interphase fraction (viable, Fig. 7b). These 2-DE maps were compared with corresponding fractions (nonviable, Fig. 7c, and viable, Fig. 7d) of enzymatically extracted cells. One clear disadvantage of the enzymatic technique was that when loss of cell viability occurred during preparation, a dramatic loss of high molecular weight polypeptides was observed (Fig. 7c). This was probably due to degradation of intracellular proteins. However, nonenzymatic preparations showed fewer differences between viable and nonviable cells: The most pronounced alteration was a decrease of a group of mucine related proteins (Fig. 7b). We conclude, therefore, that discontinuous Percoll gradient is necessary after enzymatic extraction of cells, but can be omitted from the nonenzymatic tumor sample preparation procedure.

We used the MDA-231 cell line to study the effects of cell lysis and leakage of cytosolic polypeptides during sample preparation. Remarkably, after 30, 50, 80 and 140 min of incubation in PBS/PIH at 0°C, no significant changes were observed in the 2-DE pattern (not shown). Although loss of cell viability may not result in protein degradation when cells are incubated in the presence of protease inhibitors, loss of cytosolic proteins would be expected during pelleting of cells. We monitored the loss of lactate dehydrogenase (LDH) activity into the supernatant during incubation in PBS of MDA-231 and MCF-7 breast cancer cells at 20°C. In both cases, loss of viability was paralleled by release of LDH from the cells (Fig. 8). After 5 h, 70% of the MCF-7 cells, but only 30% of the MDA-231 cells were dead (not shown).

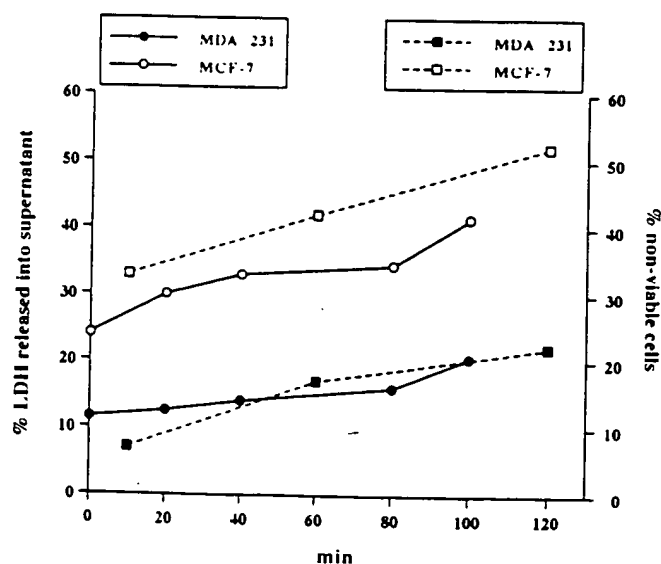


Figure 8. The relative release (fraction in supernatant of total) of lactate dehydrogenase activity (LDH) and cell viability versus incubation time of the mammary carcinoma cell lines MDA-231 and MCF-7 during incubation in PBS at 20°C.

These data indicate the impact of a rapid preparation procedure, at low temperature, of fresh tumor samples. Experiments have also been performed using only 1.07 g/mL Percoll (Fig. 6c and Fig. 1, left test tube) in order to remove erythrocytes. One clear advantage with this procedure, which today is routinely utilized, is a higher yield of viable cells, probably due to decreased sample preparation time.

4 Discussion

We describe procedures for sample preparation from solid tumors for 2-DE. 2-DE maps could be derived from solid tumors which were similar in quality to those obtained from cultured cells. Compared to methods using frozen material, the resolving power of the 2-DE technique is increased, allowing examination of a large number of polypeptides from tumors of different malignancies. Other investigators [12,22] have used samples from frozen tumors to derive 2-DE maps. We have previously described disadvantages encountered using frozen tumor samples including variations in contaminating proteins between different samples [3]. The methods described here are based on the preparation of cells from tumors without enzymatic digestion. The enzymatic step could be avoided since malignant cells usually grow as solid masses which are not strongly attached to the matrix. Furthermore, we found that omitting the enzymatic digestion alleviated the necessity of purifying viable tumor cells on Percoll gradients. This was in sharp contrast to enzymatically treated samples, where loss of viability leads to loss of high molecular weight proteins (Fig. 7c).

At least in the case of lung cancer, viable and nonviable cells showed small differences in respect to 2-DE maps. Presumably, protease inhibitors penetrate cells and inhibit proteolysis. In model experiments, we observed leakage of cytosolic protein (LDH) from the cells in parallel to loss of viability. Apparently, however, only a limited decrease of the level of low molecular weight cytosolic polypeptides was detected using silver staining combined with visual inspection. We have found that although some tumors are well suited for the preparation procedure described, others are not. In general, good results were obtained using tumors of the lung, breast, corpus and lymphomas. In contrast, cells from thyroid adenomas and hypernephroma showed poor viability. We were in these cases unable to separate nonviable cells from viable cells, and we can therefore not evaluate the consequence of the loss of viability on 2-DE patterns, apart from a loss of some low molecular weight cytosolic polypeptides.

Highly differentiated tumors may show lower viability as compared with poorly differentiated tumors (Dr. Farkas Vanky, personal communication). A number of samples from thyroid tumors were prepared for 2-DE but most cases showed poor viability. We believe that special care is needed during preparation of generally highly differentiated tumor groups. The difference between loss of viability/leakage of LDH of the more differentiated MCF-7 cells and the less differentiated MDA-231 cells is in line

with these observations (Fig. 8). A number of potential and interesting markers, like tropomyosin isoforms, cyto-keratins and heat shock proteins, appear to be insensitive to loss of viability during the preparation procedure. We have to date made numerous observations of alterations in the expression of these polypeptides in breast cancers and lung cancers.

Another problem that may occur, irrespective of sample preparation techniques used, is admixture of lymphocytes. These cases are easily detectable in smears and it may therefore be possible to select lymphocyte specific spots as "internal markers" for the 2-D PAGE analysis. Studies using this approach are in progress. Many of the polypeptides identified are structural (Table 1). Since the expression of many of these polypeptides are known to vary between normal and malignant cells, the possibility to determine their expression simultaneously is appealing. In the specific case of breast cancer, alterations in the expression of intermediate filament proteins (cytokeratins) are known to occur during tumor progression [23]. Other proteins known to be differentially expressed between normal cells and transformed cells are tropomyosins, numatrin/B23, heat shock proteins and PCNA. To this end, we have observed alterations in the expression of cytokeratin 8, hsp 90, and non-muscle tropomyosin isoform 2 during malignant progression. (Okuzawa *et al.*, in preparation and Franzén *et al.*, in preparation).

The method of choice for sample preparation from tumor tissues will depend on the properties of the tumor material studied. It may be important to use only one method when comparing cases within one group, as differences were observed between methods. The advantages of the nonenzymatic techniques are (i) that it minimizes contamination with connective tissue, (ii) that problems with contamination of serum proteins are avoided, and (iii) that separation of viable and dead cells is not necessary. Hereby the revolving power of 2-D PAGE is maximized for the analysis of human tumors and studies on inter-tumor variations in gene expression are facilitated. In addition, the polypeptide patterns obtained may be more representative for the *in vivo* tumor cell since the use of enzymes and incubations have been minimized.

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